

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,530  
Source: PG  
Date Processed by STIC: 2/2/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/524,530

TIME: 12:58:56

Input Set : A:\2005-09-29 1599-0275PUS1.ST25.txt

Output Set: N:\CRF4\02022006\J524530.raw

```

3 <110> APPLICANT: Sang-Seok KOH
4   Qing LIU
5   Hyun-Ho CHUNG
6   Wen ZENG
7   Bog-Man LEE
8   Si-Young SONG
10 <120> TITLE OF INVENTION: GENE FAMILIES ASSOCIATED WITH LIVER CANCER
12 <130> FILE REFERENCE: 1599-0275PUS1
14 <140> CURRENT APPLICATION NUMBER: US 10/524,530
15 <141> CURRENT FILING DATE: 2005-02-11
17 <150> PRIOR APPLICATION NUMBER: US 60/402,905
18 <151> PRIOR FILING DATE: 2002-08-14
20 <150> PRIOR APPLICATION NUMBER: US 60/403,651
21 <151> PRIOR FILING DATE: 2002-08-16
23 <160> NUMBER OF SEQ ID NOS: 10
25 <170> SOFTWARE: KopatentIn 1.71
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 578
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (155)..(418)
35 <223> OTHER INFORMATION: Gene LBFL302, Clone BC4
38 <400> SEQUENCE: 1
39 cggacgcgtg ggttcgaacg ttcggactga ggtttttctg cctgaagaag cgtcatcagg      60
41 accggattgt tttcgtggc ccagtgtccc cggagcttgt gtgcgataca gagagcacct      120
43 cggaagctga ggcagctggt acttgacaga gagg          atg gcg ctg tcg acc      169
44                                     Met Ala Leu Ser Thr
45                                     1          5
47 ata gtc tcc cag agg aag cag ata aag cgg aag gct ccc cgt ggc ttt      217
48 Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe
49          10          15          20
51 cta aag cga gtc ttc aag cga aag aag cct caa ctt cgt ctg gag aaa      265
52 Leu Lys Arg Val Phe Lys Arg Lys Lys Pro Gln Leu Arg Leu Glu Lys
53          25          30          35
55 agt ggt gac tta ttg gtc cat ctg aac tgt tta ctg ttt gtt cat cga      313
56 Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu Leu Phe Val His Arg
57          40          45          50
59 tta gca gaa gag tcc agg aca aac gct tgt gcg agt aaa tgt aga gtc      361
60 Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala Ser Lys Cys Arg Val
61          55          60          65
63 att aac aag gag cat gta ctg gcc gca gca aag gta att cta aag aag      409

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64 Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys Val Ile Leu Lys Lys
65 70 75 80 85
67 agc aga ggt ta gaagtcaaag aacatattct tgaaagttat gatgcattct 460
68 Ser Arg Gly
70 tttgggtggg aacagatcat aaagacattt ttacacatc agttaatatg ggattattaa 520
72 atattggcta taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 578
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 88
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapiens
80 <400> SEQUENCE: 2
81 Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys
82 1 5 10 15
84 Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys Arg Lys Lys Pro Gln
85 20 25 30
87 Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu
88 35 40 45
90 Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala
91 50 55 60
93 Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys
94 65 70 75 80
96 Val Ile Leu Lys Lys Ser Arg Gly
97 85
100 <210> SEQ ID NO: 3
101 <211> LENGTH: 531
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <220> FEATURE:
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (139)..(402)
108 <223> OTHER INFORMATION: Gene LBFL302, Clone BC7
111 <400> SEQUENCE: 3
112 ccacgcgctc cggaggtttt tctgcctgaa gaagcgtcat acggaccgga ttgttttcgc 60
114 tggcccagtg tccccggagc ttgtgtgcga tacagagagc acctcggaag ctgaggcagc 120
116 tgggtacttga cagagagg atg gcg ctg tgc acc ata gtc tcc cag agg aag 171
117 Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys
118 1 5 10
120 cag ata aag cgg aag gct ccc cgt ggc ttt cta aag cga gtc ttc aag 219
121 Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys
122 15 20 25
124 cta aag aag cct caa ctt cgt ctg gag aaa agt ggt gac tta ttg gtc 267
125 Leu Lys Lys Pro Gln Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val
126 30 35 40
128 cat ctg aac tgt tta ctg ttt gtt cat cga tta gca gaa gag tcc agg 315
129 His Leu Asn Cys Leu Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg
130 45 50 55
132 aca aac gct tgt gcg agt aaa tgt aga gtc att aac aag gag cat gta 363
133 Thr Asn Ala Cys Ala Ser Lys Cys Arg Val Ile Asn Lys Glu His Val
134 60 65 70 75

```

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136 ctg gcc gca gca aag gta att cta aag aag agc aga ggt      tagaagtc      410
137 Leu Ala Ala Ala Lys Val Ile Leu Lys Lys Ser Arg Gly
138              80              85
140 aaagaacata ttcttgaaag ttatgatgca ttcttttggg tggtaacaga tcataaagac      470
142 atttttttaca catcagttaa tatgggatta ttaaattattg gatataaaaa aaaaaaaaaa      530
144 a      531
147 <210> SEQ ID NO: 4
148 <211> LENGTH: 88
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 4
153 Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys
154 1 5 10 15
156 Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys Leu Lys Lys Pro Gln
157 20 25 30
159 Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu
160 35 40 45
162 Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala
163 50 55 60
165 Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys
166 65 70 75 80
168 Val Ile Leu Lys Lys Ser Arg Gly
169 85
172 <210> SEQ ID NO: 5
173 <211> LENGTH: 2067
174 <212> TYPE: DNA
175 <213> ORGANISM: Homo sapiens
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (32)..(1384)
180 <223> OTHER INFORMATION: Clone GE6
183 <400> SEQUENCE: 5
184 cccgggctgc caggcgccca gctgtgccca g atg gat ggg aca gag      46
185 Met Asp Gly Thr Glu
186 1 5
188 acc cgg cag cgg agg ctg gac agc tgt ggc aag cca ggg gag ctg ggg      94
189 Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys Pro Gly Glu Leu Gly
190 10 15 20
192 ctt cct cac ccc ctc agc aca gga gga ctc cct gta gcc tca gaa gat      142
193 Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro Val Ala Ser Glu Asp
194 25 30 35
196 gga gct ctc agg gcc cct gag agc caa agc gtg acc ccc aag cca ctg      190
197 Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val Thr Pro Lys Pro Leu
198 40 45 50
200 gag act gag cct agc agg gag acc gcc tgg tcc ata ggc ctt cag gtg      238
201 Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser Ile Gly Leu Gln Val
202 55 60 65
204 acc gtg ccc ttc atg ttt gca ggc ctg gga ctg tcc tgg gcc ggc atg      286
205 Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu Ser Trp Ala Gly Met

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206	70				75				80				85				
208	ctt	ctg	gac	tat	ttc	cag	gcc	aac	act	gga	caa	att	gat	gac	ccc	cag	334
209	Leu	Leu	Asp	Tyr	Phe	Gln	Ala	Asn	Thr	Gly	Gln	Ile	Asp	Asp	Pro	Gln	
210					90				95				100				
212	gag	cag	cac	aga	gtc	atc	agc	agc	aac	ctg	gcc	ctc	atc	cag	gtg	cag	382
213	Glu	Gln	His	Arg	Val	Ile	Ser	Ser	Asn	Leu	Ala	Leu	Ile	Gln	Val	Gln	
214				105					110				115				
216	gcc	act	gtc	gtg	ggg	ctc	ttg	gct	gct	gtg	gct	gcg	ctg	ctg	ttg	ggc	430
217	Ala	Thr	Val	Val	Gly	Leu	Leu	Ala	Ala	Val	Ala	Ala	Leu	Leu	Leu	Gly	
218			120					125					130				
220	gtg	gtg	tct	cga	gag	gaa	gtg	gat	gtc	gcc	aag	gtg	gag	ttg	ctg	tgt	478
221	Val	Val	Ser	Arg	Glu	Glu	Val	Asp	Val	Ala	Lys	Val	Glu	Leu	Leu	Cys	
222		135					140					145					
224	gcc	agc	agt	gtc	ctc	act	gcc	ttc	ctt	gca	gcc	ttt	gcc	ctg	ggg	gtg	526
225	Ala	Ser	Ser	Val	Leu	Thr	Ala	Phe	Leu	Ala	Ala	Phe	Ala	Leu	Gly	Val	
226	150				155					160					165		
228	ctg	atg	gtc	tgt	ata	gtg	att	ggg	gct	cga	aag	ctc	ggg	gtc	aac	cca	574
229	Leu	Met	Val	Cys	Ile	Val	Ile	Gly	Ala	Arg	Lys	Leu	Gly	Val	Asn	Pro	
230				170					175				180				
232	gac	aac	att	gcc	acg	ccc	att	gca	gcc	agc	ctg	gga	gac	ctc	atc	aca	622
233	Asp	Asn	Ile	Ala	Thr	Pro	Ile	Ala	Ala	Ser	Leu	Gly	Asp	Leu	Ile	Thr	
234			185					190				195					
236	ctg	tcc	att	ctg	gct	ttg	ggt	agc	agc	ttc	ttc	tac	aga	cac	aaa	gat	670
237	Leu	Ser	Ile	Leu	Ala	Leu	Val	Ser	Ser	Phe	Phe	Tyr	Arg	His	Lys	Asp	
238			200					205				210					
240	agt	cgg	tat	ctg	acg	ccg	ctg	gtc	tgc	ctc	agc	ttt	gcg	gct	ctg	acc	718
241	Ser	Arg	Tyr	Leu	Thr	Pro	Leu	Val	Cys	Leu	Ser	Phe	Ala	Ala	Leu	Thr	
242		215				220						225					
244	cca	gtg	tgg	gtc	ctc	att	gcc	aag	cag	agc	cca	ccc	atc	gtg	aag	atc	766
245	Pro	Val	Trp	Val	Leu	Ile	Ala	Lys	Gln	Ser	Pro	Pro	Ile	Val	Lys	Ile	
246	230				235					240					245		
248	ctg	aag	ttt	ggc	tgg	ttc	cca	atc	atc	ctg	gcc	atg	gtc	atc	agc	agt	814
249	Leu	Lys	Phe	Gly	Trp	Phe	Pro	Ile	Ile	Leu	Ala	Met	Val	Ile	Ser	Ser	
250			250					255				260					
252	ttc	gga	gga	ctc	atc	ttg	agc	aaa	acc	ggt	tct	aaa	cag	cag	tac	aaa	862
253	Phe	Gly	Gly	Leu	Ile	Leu	Ser	Lys	Thr	Val	Ser	Lys	Gln	Gln	Tyr	Lys	
254			265					270				275					
256	ggc	atg	gcg	ata	ttt	acc	ccc	gtc	ata	tgt	ggg	ggt	ggg	aat	ctg		910
257	Gly	Met	Ala	Ile	Phe	Thr	Pro	Val	Ile	Cys	Gly	Val	Gly	Gly	Asn	Leu	
258			280					285				290					
260	gtg	gcc	att	cag	acc	agc	cga	atc	tca	acc	tac	ctg	cac	atg	tgg	agt	958
261	Val	Ala	Ile	Gln	Thr	Ser	Arg	Ile	Ser	Thr	Tyr	Leu	His	Met	Trp	Ser	
262		295				300						305					
264	gca	cct	ggc	gtc	ctg	ccc	ctc	cag	atg	aag	aaa	ttc	tgg	ccc	aac	ccg	1006
265	Ala	Pro	Gly	Val	Leu	Pro	Leu	Gln	Met	Lys	Lys	Phe	Trp	Pro	Asn	Pro	
266	310				315					320			325				
268	tgt	tct	act	ttc	tgc	acg	tca	gaa	atc	aat	tcc	atg	tca	gct	cga	gtc	1054
269	Cys	Ser	Thr	Phe	Cys	Thr	Ser	Glu	Ile	Asn	Ser	Met	Ser	Ala	Arg	Val	
270				330				335				340					

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272 ctg ctg ttg ctg gtg gtc cca ggc cat ctg att ttc ttc tac atc atc      1102
273 Leu Leu Leu Leu Val Val Pro Gly His Leu Ile Phe Phe Tyr Ile Ile
274          345          350          355
276 tac ctg gtg gag ggt cag tca gtc ata aac agc cag acc ttt gtg gtg      1150
277 Tyr Leu Val Glu Gly Gln Ser Val Ile Asn Ser Gln Thr Phe Val Val
278          360          365          370
280 ctg tac ctg ctg gca ggc ctg atc cag gtg aca atc ctg ctg tac ctg      1198
281 Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr Ile Leu Leu Tyr Leu
282          375          380          385
284 gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc ctg gat cct gac      1246
285 Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala Leu Asp Pro Asp
286 390          395          400          405
288 aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac ctg ctg ggt act      1294
289 Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp Leu Leu Gly Thr
290          410          415          420
292 ggc ctg ctg gca ctg tgc ttt ttc act gac tgg cta ctg aag agc aag      1342
293 Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp Leu Leu Lys Ser Lys
294          425          430          435
296 gca gag ctg ggt ggc atc tca gaa ctg gca tct gga cct ccc taactg      1390
297 Ala Glu Leu Gly Gly Ile Ser Glu Leu Ala Ser Gly Pro Pro
298          440          445          450
300 ggccccgctg gtccatttg ctccattagaa tttcctctca catcagtggg atacagaatt      1450
302 cagttttctcc cttgccaggt ccttgggatg gttgaccctt gcctctgcag tagccttttg      1510
304 tgagtctgct aaggtagctc tcacacacct cggctctggg gttgatacct gagcctgcaa      1570
306 tagagccctg aaatcaagag catggcttga gtgtgtgaat atgatgtgtg cacatgctta      1630
308 atgagcgtgc aagtgtgcac acgtttgttg agaggagggt gttctggcct gagaaggtaa      1690
310 agaagaggca tgtccagtat gctttgcagg gtgtgtttgc tcttttccat gcccatgcaa      1750
312 cccagatttg ggtggagcag gaaggagctc ttttctgttc ccaagcctca gaactcttga      1810
314 gctgtggctt acttgcgtgc ttcaccaggt tcaagctccg tgggccacac tgctgctgtg      1870
316 ccaagaaggt gtacagcctc cccaggatgg ggccctcatc aacccttcat ctgcactcaa      1930
318 catttaatcg tgccttgcgt gtctttttat tttccttttt gtttgtttagc aaaaacctct      1990
320 atttagattt caataatcag agaagtgtaa aataaaacag atttatattgt aaaaaaaaaa      2050
322 aaaaaaaaaa aaaaaaa      2067
325 <210> SEQ ID NO: 6
326 <211> LENGTH: 451
327 <212> TYPE: PRT
328 <213> ORGANISM: Homo sapiens
330 <400> SEQUENCE: 6
331 Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys
332 1          5          10          15
334 Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
335          20          25          30
337 Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
338          35          40          45
340 Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
341          50          55          60
343 Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
344 65          70          75          80
346 Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln Ala Asn Thr Gly Gln

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**VERIFICATION SUMMARY**

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